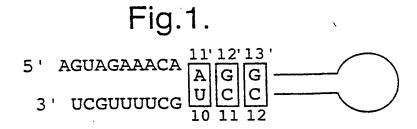
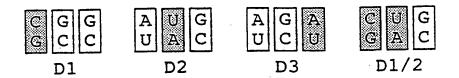
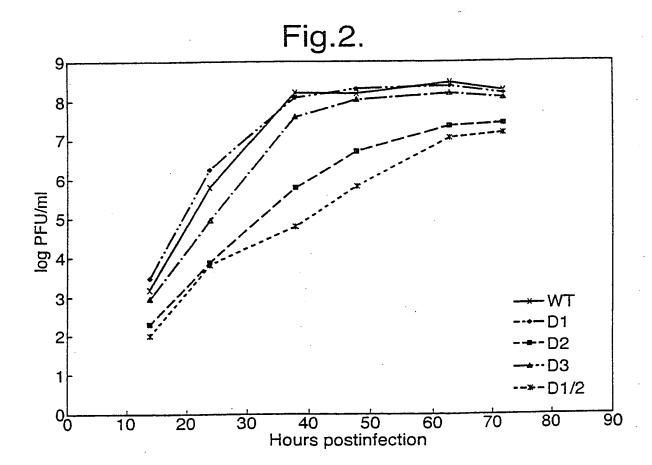
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PCT/GB99/01413

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Fig.3.

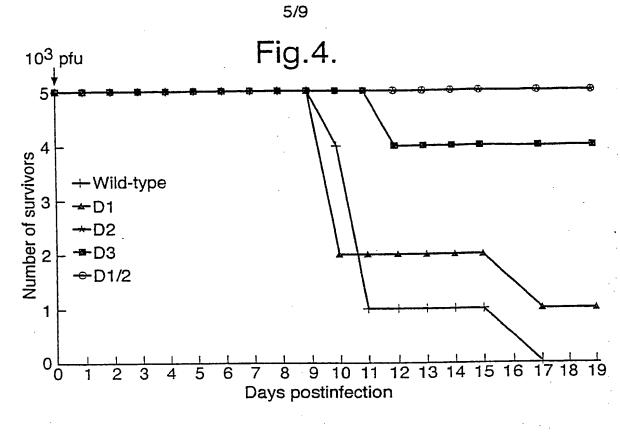
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101	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC
151	AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC
201	CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC
251	CGACAGGACT	ATAAAGATAC	CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG
301	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	GGATACCTGT	CCGCCTTTCT
351	CCCTTCGGGA	AGCGTGGCGC	TTTCTCATAG	CTCACGCTGT	AGGTATCTCA
401	GTTCGGTGTA	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC
451	GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA
501	CCCGGTAAGA	CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA
551	TTAGCAGAGC	GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG
601	CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	GCGCTCTGCT
651	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	TCCGGCAAAC
701	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG
751	CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC
801	TGACGCTCAG	TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT
851	TATCAAAAAG	GATCTTCACC	TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT
901	AAATCAATCT	AAAGTATATA	TGAGTAAACT	TGGTCTGACA	GTTACCAATG
951	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	CGTTCATCCA
1001	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA
1051	CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC
1101	TCCAGATTTA	TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA
1151	GTGGTCCTGC	AACTTTATCC	GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG
1201	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	AGTTTGCGCA	ACGTTGTTGC
1251	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	ATGGCTTCAT
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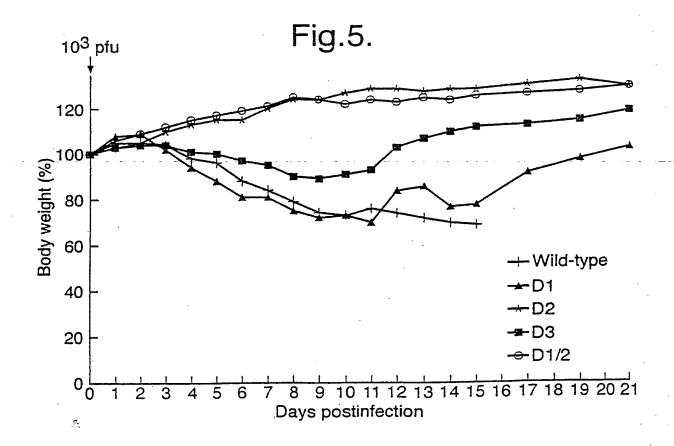
Fig.3 (Cont i).

			V . – /		
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1401	GTTGGCCGCA	GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC
1451	TTACTGTCAT	GCCATCCGTA	AGATGCTTTT	CTGTGACTGG	TGAGTACTCA
1501	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	CGACCGAGTT	GCTCTTGCCC
1551	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	TTAAAAGTGC
1601	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG
1651	CTGTTGAGAT	CCAGTŢCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC
1701	AGCATCTTTT	ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC
1751	AAAATGCCGC	AAAAAAGGGA	ATAAGGGCGA	CACGGAAATG	TTGAATACTC
1801	ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	ATTTATCAGG	GTTATTGTCT
1851	CATGAGCGGA	TACATATTTG	AATGTATTTA	GAAAAATAAA	CAAATAGGGG
1901	TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTCTA	AGAAACCATT
1951	ATTATCATGA	CATTAACCTA	TAAAAATAGG	CGTATCACGA	GGCCCTTTCG
2001	TCTCGCGCGT	TTCGGTGATG	ACGGTGAAAA	CCTCTGACAC	ATGCAGCTCC
2051	CGGAGACGGT	CACAGCTTGT	CTGTAAGCGG	ATGCCGGGAG	CAGACAAGCC
2101	CGTCAGGGCG	CGTCAGCGGG	TGTTGGCGGG	TGTCGGGGCT	GGCTTAACTA
2151	TGCGGCATCA	GAGCAGATTG	TACTGAGAGT	GCACCATATG	CGGTGTGAAA
2201	TACCGCACAG	ATGCGTAAGG	AGAAAATACC	GCATCAGGCG	CCATTCGCCA
2251	TTCAGGCTGC	GCAACTGTTG	GGAAGGGCGA	TCGGTGCGGG	CCTCTTCGCT
2301	ATTACGCCAG	CTGGCGAAAG	GGGGATGTGC	TGCAAGGCGA	TTAAGTTGGG
2351	TAACGCCAGG	GTTTTCCCAG	TCACGACGTT	GTAAAACGAC	GGCCAGTGAA
2401	TTCGAAGACG	CAGCAAAAGC	AGGAGTTTAA	ATGAATCCAA	ACCAGAAAAT
2451	AATAACCATT	GGGTCAATCT	GTATGGTAGT	CGGAATAATI	AGCCTAATAT
2501	TGCAAATAGG	; AAATATAATC	TCAATATGGA	TTAGCCATTC	AATTCAAACC
2551	GGAAATCAAA	ACCATACTGG	AATATGCAAC	CAAGGCAGCA	TTACCTATAA
2601 ⁵	AGTTGTTGCT	GGGCAGGACT	CAACTTCAGT	GATATTAACC	GGCAATTCAT
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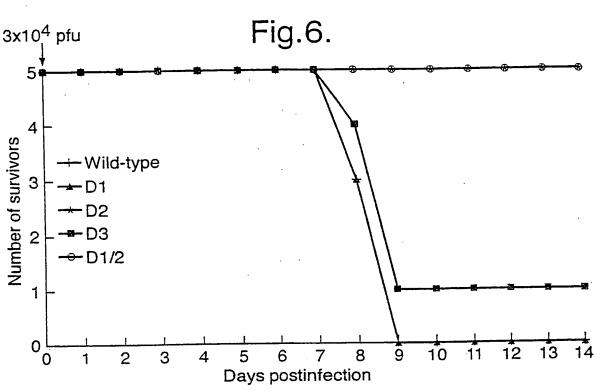
Fig.3 (Cont ii).

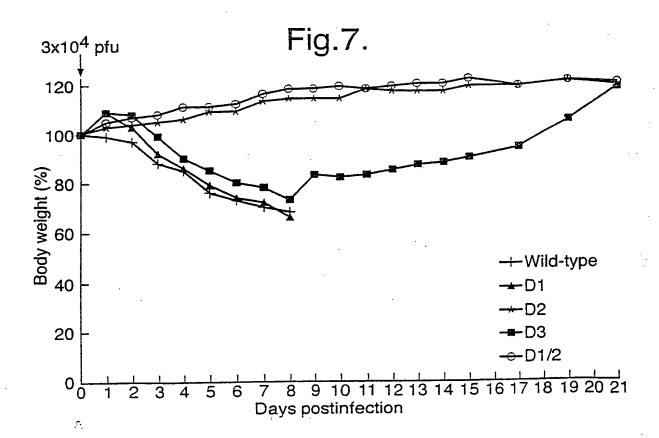
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2801	TGAATGACAA	GCATTCAAGG	GGGACCTTTA	AGGACAGAAG	CCCTTATAGG
2851	GCCTTAATGA	GCTGCCCTGT	CGGTGAAGCT	CCGTCCCCGT	ACAATTCAAG
2901	GTTTGAATCG	GTTGCTTGGT	CAGCAAGTGC	ATGTCATGAT	GGAGTGGGCT
2951	GGCTAACAAT	CGGAATTTCT	GGTCCAGATG	ATGGAGCAGT	GGCTGTATTA
3001	AAATACAACC	GCATAATAAC	TGAAACCATA	AAAAGTTGGA	GGAAGAATAT
3051	ATTGAGAACA	CAAGAGTCTG	AATGTACCTG	TGTAAATGGT	TCATGTTTTA
3101	CCATAATGAC	CGATGGCCCA	AGTGATGGGC	TGGCCTCGTA	CAAAATTTTC
3151	AAGATCGAGA	AGGGGAAGGT	TACTAAATCA	ATAGAGTTGA	ATGCACCTAA
3201	TTCTCACTAC	GAGGAATGTT	CCTGTTACCC	TGATACCGGC	AAAGTGATGT
3251	GTGTGTGCAG	AGACAATTGG	CACGGTTCGA	ACCGACCATG	GGTGTCCTTC
3301	GACCAAAACC	TAGATTATAA	AATAGGATAC	ATCTGCAGTG	GGGTTTTCGG
3351	TGACAACCCG	CGTCCCAAAG	ATGGAACAGG	CAGCTGTGGC	CCAGTGTCTG
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3451	GTTTGGATAG	GAAGGACTAA	AAGTGACAGT	TCCAGACATG	GGTTTGAGAT
3501	GATTTGGGAT	CCTAATGGAT	GGACAGAGAC	TGATAGTAGG	TTCTCTATGA
3551	GACAAGATGT	TGTGGCAATA	ACTAATCGGT	CAGGGTACAG	CGGAAGTTTC
3601.	GTTCAACATC	CTGAGCTAAC	AGGGCTAGAC	TGTATGAGGC	CTTGCTTCTG
3651	GGTTGAATTA	ATCAGGGGGC	TACCTGAGGA	GGACGCAATC	TGGACTAGTG
3701	GGAGCATCAT	TTCTTTTTGT	GGTGTGAATA	GTGATACTGT	AGATTGGTCT
3751	TGGCCAGACG	GTGCTGAGTT	GCCGTTCACC	ATTGACAAGT	AGTTTGTTCA
3801	AAAAACTCCT	TGTTTCTACT	TTTAGTGAGG	GTTAATAAGC	TTGGCGTAAT
3851	CATGGTCATA	GCTGTTTCCT	GTGTGAAATT	GTTATCCGCT	CACAATTCCA
3901	CACAACATAC	GAGCCGGAAG	CATAAAGTGT	AAAGCCTGGG	GTGCCTAATG
3951	AGTGAGCTAA	CTCACATTAA	TTGCGTTGCG	CTCACTGCCC	GCTTTCCAGT
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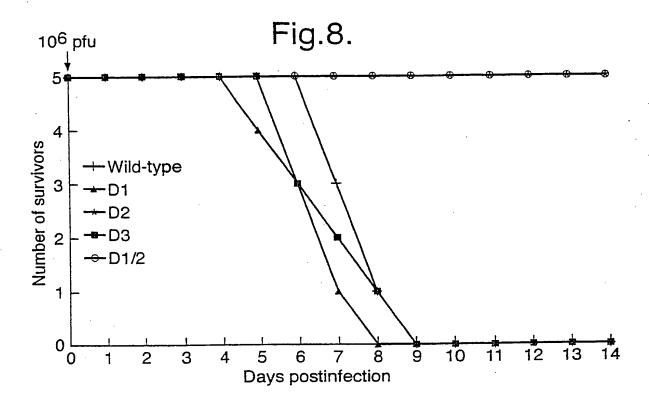


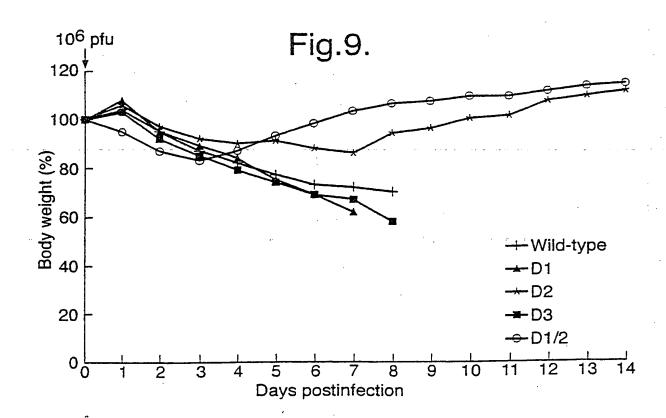


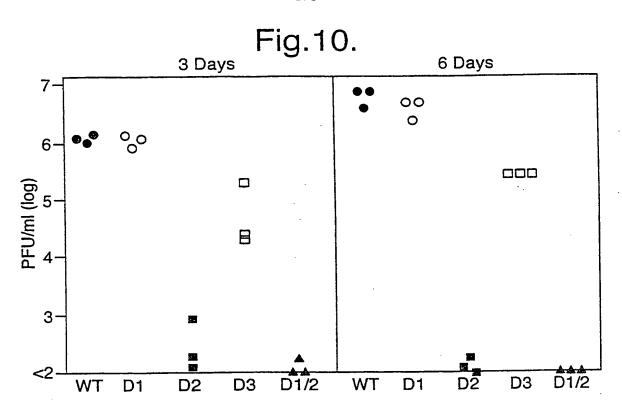
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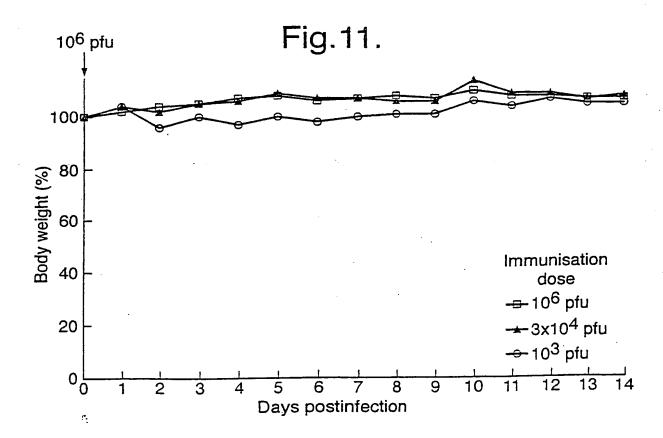












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